

## 6/10

**FIGURE 6A**

Numbering is according to Kimura et al.

## 1. 'A' Allele, CYP2D6\*3, A2637 deletion, Frameshift resulting in zero enzyme activity

5'- G C T A A C T G A G C A C A G G A T G A C C -3' NH2	CYPwt(+)/A2624, 22mer, 54%GC, Tm=63-64C	(SEQ ID NO. )
5'- G C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)/A2624(A)30-3NH2	(SEQ ID NO. )
5'- C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)/A2625(A)30-3NH2	(SEQ ID NO. )
5'- C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2	CYPwt(+)/A2625(A)30-3NH2	(SEQ ID NO. )
5'- C T A A C T G A G C A C A G G A T G A (A)30-3' NH2	CYPwt(+)/A2625(A)30-3NH2	(SEQ ID NO. )
5'- G C T A A C T G A G C A C - G G A T G A C C -3' NH2	CYPmut(+)/A2624, 21mer, 57%GC, Tm=61-63C	(SEQ ID NO. )
5'- G C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)/A2624(A)30-3NH2	(SEQ ID NO. )
5'- C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2	CYPmut(+)/A2625(A)30-3NH2	(SEQ ID NO. )
5'- C T A A C T G A G C A C - G G A T G A C (A)30-3' NH2	CYPmut(+)/A2625(A)30-3NH2	(SEQ ID NO. )
5'- C T A A C T G A G C A C - G G A T G A (A)30-3' NH2	CYPmut(+)/A2625(A)30-3NH2	(SEQ ID NO. )
5'- g c t a a c t g a g c a c a g g a t g (A)30-3' NH2	CYPwt(+)/A2624tb(A)30-3NH2	(SEQ ID NO. )
NH2 3-(A)30 g a t t g a c t c g t g t c c t a c t g -5'	CYPwt(-)/A2625(A)30-3NH2	(SEQ ID NO. )
x= 2-Amino-dA		
x= C-5 propynyl-C		
-2612		
x= C-5 propynyl-C		
5'- G C T G G A T G A G C T G C T A A C T G A G C A C A G G A T G A C C C T G G G A C C C A G C C C A G C C -3'	Wild Type (+)	(SEQ ID NO. )
5'- G C T G G A T G A G C T G C T A A C T G A G C A C - G G A T G A C C C T G G G A C C C A G C C C A G C C -3'	Mut (+)	(SEQ ID NO. )

## FIGURE 6B

3. 'C' Allele, CYP2D6*9, G2702-A2704 deletion, decreased enzyme activity		
-1909		
NH2 3-(A)30	NH2 3- G G G T C C C T G C G G G G A A A G -5'	CYPmut(-)B1930-17mer, 71%GC, Tm=56C (SEQ ID NO. )
5'- C C C A A G A C G G C C C T T T C -3'NH2	CYPmut(+)-B1930(A)30-3'NH2 (SEQ ID NO. )	
5'- C C C A A G A C G G C C C T T T C -3'NH2	CYPmut(+)-B1930(A)30-3'NH2 (SEQ ID NO. )	
5'- C C C T T A C C C C G C A T C T C C C A C C C C C A G G A C G G C C C T T T C G C C C C A A C G G T C T -3'	Wild Type (+) (SEQ ID NO. )	
	Mut (+) (SEQ ID NO. )	

 -2676	5'-G C A G A G A T G G A G A G G T G A G A G -3' NH2	CYPwlf(+)-C2691,22mer,55%GC, Tm=60C (SEQ ID NO. )
	5'-G C A G A G A T G G A G A G G T G A G A G (A)30-3' NH2	CYPwlf(+)-C2691(A)30-3NH2 (SEQ ID NO. )
	5'-C A G A G A T G G A G A G G T G A G A G (A)30-3' NH2	CYPwlf(+)-C2692(A)30-3NH2 (SEQ ID NO. )
	5'-G C A G A G A G A T G G A - - G G T G A G A G T G -3' NH2	CYPmut(+)-C2691,21mer,57%GC, Tm=60C (SEQ ID NO. )
	5'-G C A G A G A T G G A - - G G T G A G A G T G (A)30-3' NH2	CYPmut(+)-C2691(A)30-3NH2 (SEQ ID NO. )
	5'-C A G A G A T G G A - - G G T G A G A G T G (A)30-3NH2	CYPmut(+)-C2692(A)30-3NH2 (SEQ ID NO. )
	3'-T G A C T C C G G A A G G A C C G T C T C A C T C C T C A C C T - - C C A C T C T C A C C G A C G G T G C C A C -5' Wild Type (-)	(SEQ ID NO. )
	3'-T G A C T C C G G A A G G A C C G T C T C A C C T C T A C C T - - C C A C T C T C A C C G A C G G T G C C A C -5' Mut (-)	(SEQ ID NO. )

**FIGURE 6C**

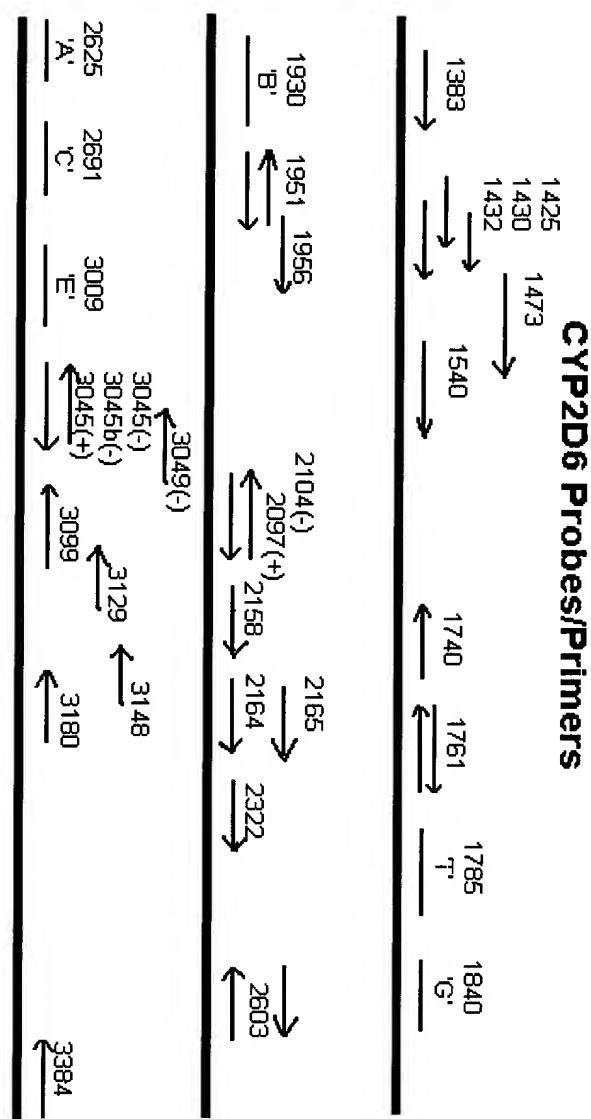
4. 'E' Allele, CYP2D6\*7, A3023C, H324P amino acid change results in zero enzyme activity.

A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) &amp; CYPmut(+)E3009 (C/A to wt at base 15)

NH2-3'-C G A G T A C T A G G A T G T A G G C -5'	CYPwt(-)E3009, 19mer, 53%GC, Pred Tm=57	(SEQ ID NO. )
NH2-3'-(A)30 C G A G T A C T A G G A T G T A G G C -5'	CYPwt(-)E3009(A)30-3'NH2	(SEQ ID NO. )
5'-G C T C A T G A T C C T A C C T C C G -3' NH2	CYPmut(+)E3009(A)30-3'NH2	(SEQ ID NO. )
5'-T G G G G C C T C C T G C T C A T G A T C C T C C G (A)30-3' NH2	CYPmut(+)E3009(A)30-3'NH2	(SEQ ID NO. )
5'-T G G G G C C T C C T G C T C A T G A T C C T C C G	Wild Type (+)	(SEQ ID NO. )
5'-T G G G G C C T C C T G C T C A T G A T C C T C C G	Mut (+)	(SEQ ID NO. )
-3038-Intron Start		
NH2-3'-G G A T G T A G G C C T A C A C G T C -5'	CYPwt(-)E3018, 19mer, 58%GC, Tm=60	(SEQ ID NO. )
5'-C C T A C A T C C G G A T G T G C A G -3'	CYPwt(-)E3018- Target	(SEQ ID NO. )
5'-C C T A C C T C C G G A T G T G C A G -3' NH2	CYPmut(+)E3018, 19mer, 63%GC, Tm=62C	(SEQ ID NO. )
3'-G G A T G G A G G C T A C A C G T C -5'	CYPmut(-)E3018- Target	(SEQ ID NO. )
5'-T G G G G C C T C C T G C T C A T G A T C C T C C G	Wild Type (+)	(SEQ ID NO. )
5'-T G G G G C C T C C T G C T C A T G A T C C T C C G	Mut (+)	(SEQ ID NO. )
-3038-Intron Start		
5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity		
1846		
5'-C A C T C C G G T G G G T G A T G G (A)30-3' NH2	CYPwt(+)-G1840(A)30-3'NH2, 18mer, 67%GC, Tm=60	(SEQ ID NO. )
NH2-3'-(A)30 G T G A G G G C C A C C C A C T A C C -5'	CYPwt(-)G1840(A)30-3'NH2	(SEQ ID NO. )
5'-C A C T C C T G T G G G T G A T G G (A)30-3' NH2	CYPmut(+)G1840(A)30-3'NH2, 18mer, 61%GC, Tm=57	(SEQ ID NO. )
5'-G T G C C G C C T T C G C C A C T C C G G T G A T G G G C A G A A G G G C A C A A G C G G G -3'	(SEQ ID NO. )	
5'-G T G C C G C C T T C G C C A C T C C G G T G A T G G G C A G A A G G G C A C A A G C G G G -3'	(SEQ ID NO. )	
Exon 3 end-1846		



Figure 7



CYPwt(+)1383, CYPwt(+)2097, CYPwt(-)2104, and CYPwt(-)3180 are published primer sequences.

1. Chen et al., Clinical Pharmacology and Therapeutics, Vol 60, 5522-34
2. Heim M, Meyer UA. Lancet 1990; 336:529-32

CYPwt(+)1540 and CYPwt(-)3099 are primers obtained from Intek, referred to as MP3 and MP4 respectively.